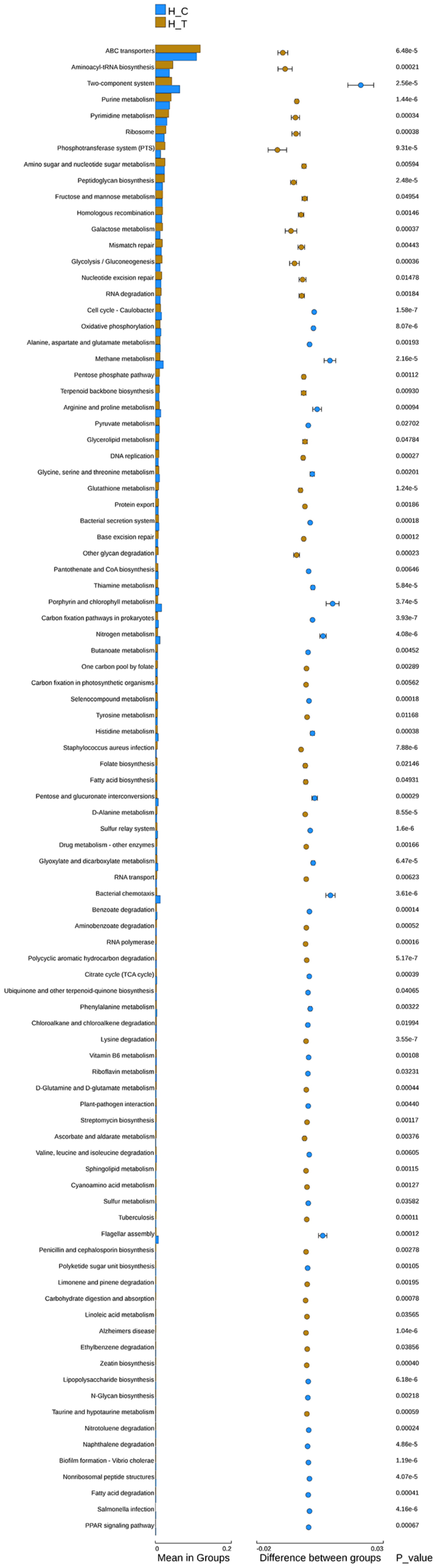
H_C
H_T
ABC transporters 6.48e-5
Aminoacyl-tRNA biosynthesis 0.00021
Two-component system 2.56e-5
Purine metabolism 1.44e-6
Pyrimidine metabolism 0.00034
Ribosome 0.00038
Phosphotransferase system (PTS) 9.31e-5
Amino sugar and nucleotide sugar metabolism 0.00594
Peptidoglycan biosynthesis 2.48e-5
Fructose and mannose metabolism 0.04954
Homologous recombination 0.00146
Galactose metabolism 0.00037
Mismatch repair 0.00443
Glycolysis / Gluconeogenesis 0.00036
Nucleotide excision repair 0.01478
RNA degradation 0.00184
Cell cycle - Caulobacter 1.58e-7
Oxidative phosphorylation 8.07e-6
Alanine, aspartate and glutamate metabolism 0.00193
Methane metabolism 2.16e-5
Pentose phosphate pathway 0.00112
Terpenoid backbone biosynthesis 0.00930
Arginine and proline metabolism 0.00094
Pyruvate metabolism 0.02702
Glycerolipid metabolism 0.04784
DNA replication 0.00027
Glycine, serine and threonine metabolism 0.00201
Glutathione metabolism 1.24e-5
Protein export 0.00186
Bacterial secretion system 0.00018
Base excision repair 0.00012
Other glycan degradation 0.00023
Pantothenate and CoA biosynthesis 0.00646
Thiamine metabolism 5.84e-5
Porphyrin and chlorophyll metabolism 3.74e-5
Carbon fixation pathways in prokaryotes 3.93e-7
Nitrogen metabolism 4.08e-6
Butanoate metabolism 0.00452
One carbon pool by folate 0.00289
Carbon fixation in photosynthetic organisms 0.00562
Selenocompound metabolism 0.00018
Tyrosine metabolism 0.01168
Histidine metabolism 0.00038
Staphylococcus aureus infection 7.88e-6
Folate biosynthesis 0.02146
Fatty acid biosynthesis 0.04931
Pentose and glucuronate interconversions 0.00029
D-Alanine metabolism 8.55e-5
Sulfur relay system 1.6e-6
Drug metabolism - other enzymes 0.00166
Glyoxylate and dicarboxylate metabolism 6.47e-5
RNA transport 0.00623
Bacterial chemotaxis 3.61e-6
Benzoate degradation 0.00014
Aminobenzoate degradation 0.00052
RNA polymerase 0.00016
Polycyclic aromatic hydrocarbon degradation 5.17e-7
Citrate cycle (TCA cycle) 0.00039
Ubiquinone and other terpenoid-quinone biosynthesis 0.04065
Phenylalanine metabolism 0.00322
Chloroalkane and chloroalkene degradation 0.01994
Lysine degradation 3.55e-7
Vitamin B6 metabolism 0.00108
Riboflavin metabolism 0.03231
D-Glutamine and D-glutamate metabolism 0.00044
Plant-pathogen interaction 0.00440
Streptomycin biosynthesis 0.00117
Ascorbate and aldarate metabolism 0.00376
Valine, leucine and isoleucine degradation 0.00605
Sphingolipid metabolism 0.00115
Cyanoamino acid metabolism 0.00127
Sulfur metabolism 0.03582
Tuberculosis 0.00011
Flagellar assembly 0.00012
Penicillin and cephalosporin biosynthesis 0.00278
Polyketide sugar unit biosynthesis 0.00105
Limonene and pinene degradation 0.00195
Carbohydrate digestion and absorption 0.00078
Linoleic acid metabolism 0.03565
Alzheimers disease 1.04e-6
Ethylbenzene degradation 0.03856
Zeatin biosynthesis 0.00040
Lipopolysaccharide biosynthesis 6.18e-6
N-Glycan biosynthesis 0.00218
Taurine and hypotaurine metabolism 0.00059
Nitrotoluene degradation 0.00024
Naphthalene degradation 4.86e-5
Biofilm formation - Vibrio cholerae 1.19e-6
Nonribosomal peptide structures 4.07e-5
Fatty acid degradation 0.00041
Salmonella infection 4.16e-6
PPAR signaling pathway 0.00067
0
0.2
Mean in Groups
-0.02
0.03
Difference between groups
P_value